

U.S.S.N. 09/768,155
Filed: January 23, 2001
AMENDMENT

Remarks

The specification has been amended to incorporate the proper sequence listing annotations as prescribed by 37 CFR. 1.182(d). The amendments have been made pursuant to 37 CFR 1.121 including a marked up copy of the amendments and instruction, which unambiguously identifies the location, to replace the appropriate paragraphs with the amended paragraphs.

Respectfully submitted,



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Certificate of Facsimile Transmission

I hereby certify that this Amendment and Response to Office Action, and any documents referred to as attached therein are being facsimile transmitted on this date, to the Commissioner for Patents, U.S. Patent and Trademark Office, Washington, DC 20231.

Jean Hicks

Date: December 2, 2002

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MARKED UP VERSION OF SPECIFICATION PURSUANT TO 37 C.F.R. § 1.121

Marked Up Version of Amended Specification Paragraphs**Pursuant to 37 C.F.R. § 1.121(b)(1)(iii)**

-- Figures 2a and 2b are the nucleotide (SEQ ID NO:1) and deduced amino acid (SEQ ID NO:2) sequences of the cDNA insert in G7. Asterisks show the stop codon. This sequence has been added to the GenBank nucleic acid sequence database, Los Alamos National Laboratory, NM, and has been assigned accession number U27517. --

-- Figure 3a and 3b are an alignment of the central core regions of 5 ribosomal proteins (SEQ ID NOS:3 to 7)(r-proteins) S1. Asterisks show the 5 repeating regions (SEQ ID NOS:8 to 12)(a, b, c, d, and e, respectively). Spaces indicate positions where gaps were introduced to optimize alignment of the sequences (SEQ ID NOS:3 to 7). Dashes indicate identity to the residues of HS1 (SEQ ID NO:3). Alignment of the central core region of HS1 (SEQ ID NO:3) is residues 63-317. HS1; human r-protein S1 (SEQ ID NO:3) presented in this study, ES1; E. coli r-protein S1 (SEQ ID NO:4)(Ref. 26), RS1; Rhizobium meliloti r-protein S1 (SEQ ID NO:5)(Ref. 28), PS1, Providencia sp. r-protein S1 (SEQ ID NO:6)(Ref. 27), CS1; chloroplast r-protein S1 (SEQ ID NO:7)(Ref. 29).--

-- Although described herein with reference to the whole protein, it is preferable to use peptides of between a few amino acids up to about 100 amino acids, more preferably less than forty amino acids, still more preferably less than ten to twenty amino acids. These peptides can be easily ascertained by immobilizing the anti-dsDNA antibodies from a patient(s) and screening for binding of the peptides. Peptides can be prepared using standard techniques for amino acid synthesis or recombinantly, by engineering the cDNA (SEQ ID NO:1) encoding the protein, described in Figures 2a and 2b.--

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-- The nucleotide sequence of the cDNA insert in G7 was determined. Its primary nucleotide (SEQ ID NO:1) and deduced amino acid (SEQ ID NO:2) sequences (GenBank no. U27517) are shown in Figures 2a and 2b. The cDNA insert (SEQ ID NO:1) proved to be 1,314 nucleotides in length. The TAA stop codon is located at positions 1057-1059. The predicted molecular weight for the encoded polypeptides (SEQ ID NO:2) (352 amino acids) is 38.0 kDa. However, this cDNA insert (SEQ ID NO:1) in G7 seems to be a partial length cDNA because the molecular weight of the encoded polypeptide (SEQ ID NO:2) is smaller than the estimated full length size (104 kDa) of the reactive protein in MOLT4 cell extract. Thus, this cDNA (SEQ ID NO:1) does not seem to contain the initiation codon.--

-- A search for similarities between the nucleotide sequence of the cDNA (SEQ ID NO:1) in G7 (GenBank no. U27517) and other sequences through the NCBI using [he] the BLAST network service showed a significant match (99% identity) with a sequence encoding human ribosomal protein (r-protein) S1 homologue mRNA reported by Eklund et al., *Gene* 155:231 (1995) (SEQ ID NO:3). However, there are 3 nucleotide and 1 amino acid differences between the G7 cDNA insert (SEQ ID NO:1) and their cDNA sequence (SEQ ID NO:3) (GTC (positions 130-132) in the G7 cDNA insert (SEQ ID NO:1) vs GTA (positions 292-294) in their cDNA (SEQ ID NO:3), AGT (positions 133-135, encodes Ser at residue 45) in the G7 cDNA insert (SEQ ID NO:1) vs GCT (positions 295-297, encodes Ala at residue 99) in their cDNA (SEQ ID NO:3)]. Moreover, 2 nucleotides (C at positions 1355 and 1366) and 162 nucleotides (positions 1-162) in their cDNA (SEQ ID NO:3) are deleted in the G7 cDNA insert (SEQ ID NO:1). A search was made for some similarities between the predicted amino acid sequence (SEQ ID NO:2) and other protein sequences in the SWISSPROT database using the algorithm as described by